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W069: Banana (Musa) Genomics

Sequencing The Banana Genome

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Bananas (Musa) are the fourth most important crop in developing countries. They are important as an export crop but also play a major role in local food security. Crops of Musa are susceptible to an ever increasing range of diseases requiring massive use of pesticides that have dramatic environmental and health impacts and threaten the sustainability of the crop. There is thus an urgent need for a wider diversity of genetically improved banana cultivars with more robust disease resistance, increased productivity and better adaptability to a large range of growing conditions. The production of export dessert bananas relies on very few related genotypes of the Cavendish subgroup with an AAA genome constitution. However, numerous dessert and cooking types with an AAA, AAB (including plantain) or ABB genome constitution are grown for local consumption. The Musa accession selected for sequencing is a doubled haploid of the accession ‘Pahang’ (DH Pahang). This accession belongs to the Musa acuminata species (AA genome) malaccensis subspecies. We generated 20x coverage using paired and single 454 reads, complemented by Sanger BESs and ~50 x coverage of Illumina shotgun data. The assembly was performed with Newbler, and the scaffolds were anchored to a genetic map. Genes were predicted using a reconciliation approach taking ESTs, protein sequences and ab initio data as input. A genetic map of the parent accession ‘Pahang’ was developed with SSR and DArT markers to assemble the scaffolds in pseudo-molecules.